

#10

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Applicant (s): Kitisri Sukhapinda et al.

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For: ANTIBODY-MEDIATED DOWN-REGULATION OF PLANT PROTEINS

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Washington, DC 20231

Sir:

STATEMENT PURSUANT TO 37 CFR 1.821(f)
VERIFYING SEQUENCE SUBMISSION

The information recorded in the computer readable form is identical to the
written sequence listing.

Respectfully submitted,

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<120> ANTIBODY-MEDIATED DOWN-REGULATION OF PLANT PROTEINS

<130> 50447

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<150> US 60/093,587

<151> 1998-07-21

<160> 56

<170> PatentIn Ver. 2.0

<210> 1

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:5' primer

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17

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1 5 10 15

48

ggg agg gtg gat atg agg cag att gag aag aca att cag tat ctt att

96

Gly	Arg	Val	Asp	Met	Arg	Gln	Ile	Glu	Lys	Thr	Ile	Gln	Tyr	Leu	Ile		
			20					25					30				
ggc	tct	gga	atg	gat	cct	agg	act	gag	aat	aat	cct	tat	ctt	ggt	ttc	144	
Gly	Ser	Gly	Met	Asp	Pro	Arg	Thr	Glu	Asn	Asn	Pro	Tyr	Leu	Gly	Phe		
		35					40					45					
atc	tac	acc	tcc	ttc	caa	gag	cgg	gcg	acc	ttc	atc	tca	cac	ggg	aac	192	
Ile	Tyr	Thr	Ser	Phe	Gln	Glu	Arg	Ala	Thr	Phe	Ile	Ser	His	Gly	Asn		
	50					55					60						
act	gct	cgt	cac	gcc	aag	gac	ttt	ggc	gac	tta	aag	ctt	gca	caa	atc	240	
Thr	Ala	Arg	His	Ala	Lys	Asp	Phe	Gly	Asp	Leu	Lys	Leu	Ala	Gln	Ile		
	65				70					75					80		
tgc	ggc	atc	atc	gcc	tca	gat	gag	aag	cga	cat	gaa					276	
Cys	Gly	Ile	Ile	Ala	Ser	Asp	Glu	Lys	Arg	His	Glu						
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			20					25					30				
Gly	Ser	Gly	Met	Asp	Pro	Arg	Thr	Glu	Asn	Asn	Pro	Tyr	Leu	Gly	Phe		
		35					40					45					
Ile	Tyr	Thr	Ser	Phe	Gln	Glu	Arg	Ala	Thr	Phe	Ile	Ser	His	Gly	Asn		
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Thr	Ala	Arg	His	Ala	Lys	Asp	Phe	Gly	Asp	Leu	Lys	Leu	Ala	Gln	Ile		
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gtcccccttc ccattggcct ccacg atg gcg ctc cgc ctc aac gac gtc gcg 172
Met Ala Leu Arg Leu Asn Asp Val Ala
-30 -25
ctc tgc ctc tcc ccg ccg ctc gcc gcc cgc cgc cgc cgc cgc agc agc 220
Leu Cys Leu Ser Pro Pro Leu Ala Ala Arg Arg Arg Arg Arg Ser Ser
-20 -15 -10
ggc agg ttc gtc gcc gtc gcc tcc atg acg tcc gcc gtc tcc acc aag 268
Gly Arg Phe Val Ala Val Ala Ser Met Thr Ser Ala Val Ser Thr Lys
-5 -1 1 5 10
gtc gag aat aag aag cca ttt gct cct cca agg gag gta cat gtc cag 316
Val Glu Asn Lys Lys Pro Phe Ala Pro Arg Glu Val His Val Gln
15 20 25
gtt aca cat tca atg cca cct cac aag att gaa att ttc aag tcg ctt 364
Val Thr His Ser Met Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu
30 35 40
gat gat tgg gct aga gat aat atc ttg acg cat ctc aag cca gtc gag 412
Asp Asp Trp Ala Arg Asp Asn Ile Leu Thr His Leu Lys Pro Val Glu
45 50 55
aag tgt tgg cag cca cag gat ttc ctc ccg gac cca gca tct gaa gga 460
Lys Cys Trp Gln Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly
60 65 70
ttt cat gat gaa gtt aag gag ctc aga gaa cgt gcc aag gaa atc cct 508
Phe His Asp Glu Val Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro
75 80 85 90
gat gat tat ttt gtt tgt ttg gtg gga gac atg att acc gag gaa gct 556
Asp Asp Tyr Phe Val Cys Leu Val Gly Asp Met Ile Thr Glu Glu Ala
95 100 105
cta cca aca tac cag act atg ctt aac acc ctc gac ggt gtc aga gat 604
Leu Pro Thr Tyr Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp
110 115 120
gag aca ggt gca agc ccc act gcc tgg gct gtt tgg acg agg gca tgg 652
Glu Thr Gly Ala Ser Pro Thr Ala Trp Ala Val Trp Thr Arg Ala Trp
125 130 135
act gct gag gag aac agg cat ggt gat ctg ctc aac aag tat atg tac 700
Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr
140 145 150
ctc act ggg agg gtg gat atg agg cag att gag aag aca att cag tat 748
Leu Thr Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr
155 160 165 170
ctt att ggc tct gga atg gat cct agg act gag aat aat cct tat ctt 796
Leu Ile Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu
175 180 185
ggt ttc atc tac acc tcc ttc caa gag cgg gcg acc ttc atc tca cac 844
Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His
190 195 200

ggg aac act gct cgt cac gcc aag gac ttt ggc gac tta aag ctt gca 892
 Gly Asn Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala
 205 210 215

caa atc tgc ggc atc atc gcc tca gat gag aag cga cat gaa act gcg 940
 Gln Ile Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala
 220 225 230

tac acc aag atc gtg gag aag ctg ttt gag atc gac cct gat ggt acc 988
 Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr
 235 240 245 250

gtg gtc gct ctg gct gac atg atg agg aag aag atc tca atg cct gcc
 1036
 Val Val Ala Leu Ala Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala
 255 260 265

cac ctg atg ttt gac ggg cag gac gac aag ctg ttc gag cac ttc tcc
 1084
 His Leu Met Phe Asp Gly Gln Asp Asp Lys Leu Phe Glu His Phe Ser
 270 275 280

atg gtc gcg cag agg ctt ggc gtt tac acc gcc agg gac tac gcc gac
 1132
 Met Val Ala Gln Arg Leu Gly Val Tyr Thr Ala Arg Asp Tyr Ala Asp
 285 290 295

atc ctc gag ttc ctc gtc gac agg tgg aag gtg gcg agc ctg act ggt
 1180
 Ile Leu Glu Phe Leu Val Asp Arg Trp Lys Val Ala Ser Leu Thr Gly
 300 305 310

ctg tcg ggt gaa ggg aac aag gcg cag gac tac ctt tgc acc ctt gct
 1228
 Leu Ser Gly Glu Gly Asn Lys Ala Gln Asp Tyr Leu Cys Thr Leu Ala
 315 320 325 330

tca aga atc agg agg ctg gag gag agg gcc cag agc aga gcc aag aaa
 1276
 Ser Arg Ile Arg Arg Leu Glu Glu Arg Ala Gln Ser Arg Ala Lys Lys
 335 340 345

gcc ggc acg ctg cct ttc agc tgg gta tac ggt agg gac gtc caa ctg
 1324
 Ala Gly Thr Leu Pro Phe Ser Trp Val Tyr Gly Arg Asp Val Gln Leu
 350 355 360

tgagatcgga aacctgctgc ggactgctta gacaagacct gctgtgtctg cgttacatag
 1384

gtctccaggt tttgatcaaa tgggtcccggtg tcgtcttata gagcgatagg agaactgtgt
 1444

ggtctgtggt gtagctttgt ttttattttg tatttttctg ctttgatgta caacctgtgg
 1504

ccgcatgaac tggggcggtg agatgggagc gaccatgccg tactttgtct gtcgctggcg
 1564

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1621

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<211> 393
<212> PRT
<213> Zea mays

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-15 -10 -5 -1 1
Ser Met Thr Ser Ala Val Ser Thr Lys Val Glu Asn Lys Lys Pro Phe
5 10 15
Ala Pro Pro Arg Glu Val His Val Gln Val Thr His Ser Met Pro Pro
20 25 30
His Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg Asp Asn
35 40 45
Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro Gln Asp
50 55 60 65
Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu Val Lys Glu
70 75 80
Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Cys Leu
85 90 95
Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr Met
100 105 110
Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser Pro Thr
115 120 125
Ala Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His
130 135 140 145
Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg Val Asp Met
150 155 160
Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp
165 170 175
Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe
180 185 190
Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg His Ala
195 200 205
Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile Cys Gly Ile Ile Ala
210 215 220 225
Ser Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val Glu Lys
230 235 240

Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Val Ala Leu Ala Asp Met
 245 250 255
 Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Phe Asp Gly Gln
 260 265 270
 Asp Asp Lys Leu Phe Glu His Phe Ser Met Val Ala Gln Arg Leu Gly
 275 280 285
 Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Asp
 290 295 300 305
 Arg Trp Lys Val Ala Ser Leu Thr Gly Leu Ser Gly Glu Gly Asn Lys
 310 315 320
 Ala Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg Arg Leu Glu
 325 330 335
 Glu Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu Pro Phe Ser
 340 345 350
 Trp Val Tyr Gly Arg Asp Val Gln Leu
 355 360

<210> 7
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

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<210> 8
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 <212> DNA
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 <223> Description of Artificial Sequence:primer

 <400> 8
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36

<210> 9
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

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<210> 10
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

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<210> 11
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 <212> DNA
 <213> Zea mays

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 <222> (4)..(1092)

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 Lys Pro Phe Ala Pro Pro Arg Glu Val His Val Gln Val Thr His Ser
 20 25 30
 atg cca cct cac aag att gaa att ttc aag tcg ctt gat gat tgg gct 144
 Met Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala
 35 40 45
 aga gat aat atc ttg acg cat ctc aag cca gtc gag aag tgt tgg cag 192
 Arg Asp Asn Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln
 50 55 60
 cca cag gat ttc ctc ccg gac cca gca tct gaa gga ttt cat gat gaa 240
 Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu
 65 70 75
 gtt aag gag ctc aga gaa cgt gcc aag gaa atc cct gat gat tat ttt 288
 Val Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe
 80 85 90 95
 gtt tgt ttg gtg gga gac atg att acc gag gaa gct cta cca aca tac 336
 Val Cys Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr
 100 105 110
 cag act atg ctt aac acc ctc gac ggt gtc aga gat gag aca ggt gca 384
 Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala
 115 120 125
 agc ccc act gcc tgg gct gtt tgg acg agg gca tgg act gct gag gag 432
 Ser Pro Thr Ala Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu
 130 135 140
 aac agg cat ggt gat ctg ctc aac aag tat atg tac ctc act ggg agg 480
 Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg
 145 150 155

gtg gat atg agg cag att gag aag aca att cag tat ctt att ggc tct 528
 Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser
 160 165 170 175

gga atg gat cct agg act gag aat aat cct tat ctt ggt ttc atc tac 576
 Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr
 180 185 190

acc tcc ttc caa gag cgg gcg acc ttc atc tca cac ggg aac act gct 624
 Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala
 195 200 205

cgt cac gcc aag gac ttt ggc gac tta aag ctt gca caa atc tgc ggc 672
 Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile Cys Gly
 210 215 220

atc atc gcc tca gat gag aag cga cat gaa act gcg tac acc aag atc 720
 Ile Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile
 225 230 235

gtg gag aag ctg ttt gag atc gac cct gat ggt acc gtg gtc gct ctg 768
 Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Val Ala Leu
 240 245 250 255

gct gac atg atg agg aag aag atc tca atg cct gcc cac ctg atg ttt 816
 Ala Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Phe
 260 265 270

gac ggg cag gac gac aag ctg ttc gag cac ttc tcc atg gtc gcg cag 864
 Asp Gly Gln Asp Asp Lys Leu Phe Glu His Phe Ser Met Val Ala Gln
 275 280 285

agg ctt ggc gtt tac acc gcc agg gac tac gcc gac atc ctc gag ttc 912
 Arg Leu Gly Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Leu Glu Phe
 290 295 300

ctc gtc gac agg tgg aag gtg gcg agc ctg act ggt ctg tcg ggt gaa 960
 Leu Val Asp Arg Trp Lys Val Ala Ser Leu Thr Gly Leu Ser Gly Glu
 305 310 315

ggg aac aag gcg cag gac tac ctt tgc acc ctt gct tca aga atc agg
 1008
 Gly Asn Lys Ala Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg
 320 325 330 335

agg ctg gag gag agg gcc cag agc aga gcc aag aaa gcc ggc acg ctg
 1056
 Arg Leu Glu Glu Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu
 340 345 350

cct ttc agc tgg gta tac ggt agg gac gtc caa ctg tgagctagca tcac
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 Pro Phe Ser Trp Val Tyr Gly Arg Asp Val Gln Leu
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 <211> 363
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 <213> Zea mays

<400> 12

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Asp	Asn	Ile	Leu	Thr	His	Leu	Lys	Pro	Val	Glu	Lys	Cys	Trp	Gln	Pro	
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Gln	Asp	Phe	Leu	Pro	Asp	Pro	Ala	Ser	Glu	Gly	Phe	His	Asp	Glu	Val	
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Lys	Glu	Leu	Arg	Glu	Arg	Ala	Lys	Glu	Ile	Pro	Asp	Asp	Tyr	Phe	Val	
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Cys	Leu	Val	Gly	Asp	Met	Ile	Thr	Glu	Glu	Ala	Leu	Pro	Thr	Tyr	Gln	
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Thr	Met	Leu	Asn	Thr	Leu	Asp	Gly	Val	Arg	Asp	Glu	Thr	Gly	Ala	Ser	
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Pro	Thr	Ala	Trp	Ala	Val	Trp	Thr	Arg	Ala	Trp	Thr	Ala	Glu	Glu	Asn	
		130				135						140				
Arg	His	Gly	Asp	Leu	Leu	Asn	Lys	Tyr	Met	Tyr	Leu	Thr	Gly	Arg	Val	
145					150					155					160	
Asp	Met	Arg	Gln	Ile	Glu	Lys	Thr	Ile	Gln	Tyr	Leu	Ile	Gly	Ser	Gly	
				165					170					175		
Met	Asp	Pro	Arg	Thr	Glu	Asn	Asn	Pro	Tyr	Leu	Gly	Phe	Ile	Tyr	Thr	
			180					185					190			
Ser	Phe	Gln	Glu	Arg	Ala	Thr	Phe	Ile	Ser	His	Gly	Asn	Thr	Ala	Arg	
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His	Ala	Lys	Asp	Phe	Gly	Asp	Leu	Lys	Leu	Ala	Gln	Ile	Cys	Gly	Ile	
	210					215					220					
Ile	Ala	Ser	Asp	Glu	Lys	Arg	His	Glu	Thr	Ala	Tyr	Thr	Lys	Ile	Val	
225					230					235					240	
Glu	Lys	Leu	Phe	Glu	Ile	Asp	Pro	Asp	Gly	Thr	Val	Val	Ala	Leu	Ala	
				245					250					255		
Asp	Met	Met	Arg	Lys	Lys	Ile	Ser	Met	Pro	Ala	His	Leu	Met	Phe	Asp	
			260					265					270			
Gly	Gln	Asp	Asp	Lys	Leu	Phe	Glu	His	Phe	Ser	Met	Val	Ala	Gln	Arg	
		275					280					285				
Leu	Gly	Val	Tyr	Thr	Ala	Arg	Asp	Tyr	Ala	Asp	Ile	Leu	Glu	Phe	Leu	
	290					295					300					
Val	Asp	Arg	Trp	Lys	Val	Ala	Ser	Leu	Thr	Gly	Leu	Ser	Gly	Glu	Gly	
305					310					315					320	

Asn Lys Ala Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg Arg
325 330 335

Leu Glu Glu Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu Pro
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Phe Ser Trp Val Tyr Gly Arg Asp Val Gln Leu
355 360

<210> 13
<211> 9
<212> PRT
<213> Zea mays

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<210> 14
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<212> PRT
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1 5 10

<210> 15
<211> 31
<212> PRT
<213> Zea mays

<400> 15
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1 5 10 15

Ala Ala Arg Arg Arg Arg Ser Ser Gly Arg Phe Val Ala Val
20 25 30

<210> 16
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

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42

<210> 17
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

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<210>. 18

<211> 46

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence:primer

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<210> 19

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 19

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<210> 20

 $\langle 211 \rangle$ 102

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence:primer

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cattctgcct ttgcggcggt tgtgatgacc ccaaaccac tc

<210> 21

<211> 738

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<220>

<221> CDS

<222> (37) .. (693)

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Asp Val Val Met Thr Pro
1 5

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Asn Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser

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Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu				
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cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac				198
His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr				
	40	45	50	
aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt				246
Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser				
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gga tca ggg aca gat ttc aca ctc aag atc aac aga gtg gag gct gag				294
Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Asn Arg Val Glu Ala Glu				
	75	80	85	
gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg				342
Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr				
	90	95	100	
ttc gga ggg ggg acc aag ctg gaa ata aaa cgg gct gat gct gca cca				390
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro				
	105	110	115	
act gta tcc atc ttc cca cca tcc agt gag cag tta aca tct gga ggt				438
Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly				
	120	125	130	
gcc tca gtc gtg tgc ttc ttg aac aac ttc tac ccc aaa gac atc aat				486
Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn				
	135	140	145	150
gtc aag tgg aag att gat ggc agt gaa cga caa aat ggc gtc ctg aac				534
Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn				
	155	160	165	
agt tgg act gat cag gac acc aaa gac agc acc tac agc atg agc agc				582
Ser Trp Thr Asp Gln Asp Thr Lys Asp Ser Thr Tyr Ser Met Ser Ser				
	170	175	180	
acc ctc acg ttg acc aag gac gag tat gaa cga cat aac agc tat acc				630
Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr				
	185	190	195	
tgt gag gcc act cac aag aca tca act tca ccc att gtc aag agc ttc				678
Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe				
	200	205	210	
aac agg aat gag tgt tagtaagcta gcacgcccga tgggtgggacg gtatgaataa				733
Asn Arg Asn Glu Cys				
215				
tccgg				738

<210> 22
 <211> 336
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (1)..(336)

<400> 22
 gat gtt gtg atg acc cca aac cca ctc tcc ctg cct gtc agt ctt gga 48
 Asp Val Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val Ser Leu Gly
 1 5 10 15
 gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt 96
 Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
 20 25 30
 aat gga atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct 144
 Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca 192
 Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc 240
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 aac aga gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt 288
 Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
 85 90 95
 aca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa 336
 Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 23
 <211> 108
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 23
 gcactagggtc aatctagaat ggtaagcgct attgttttat atgtgctttt ggcggcggcg 60
 ggcgattctg cctttgcggc ggttcaactg cagcagtctg gggctgag 108

<210> 24
 <211> 882
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (25)..(837)

<220>
 <221> mat_peptide
 <222> (79)..(837)

<400> 24

ctgcagggta cggccatatt ggcc atg act atc ctt tgc tgg ctg gcc ctt	51
Met Thr Ile Leu Cys Trp Leu Ala Leu	
-15 -10	
ctg tca act ctg act gcc gtc aac act gcg gtt gtg atg acc cca aac	99
Leu Ser Thr Leu Thr Ala Val Asn Thr Ala Val Val Met Thr Pro Asn	
-5 -1 1 5	
cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc	147
Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys	
10 15 20	
aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta cat	195
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His	
25 30 35	
tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa	243
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys	
40 45 50 55	
gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga	291
Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly	
60 65 70	
tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat	339
Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp	
75 80 85	
ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc	387
Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe	
90 95 100	
gga ggg ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc	435
Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly	
105 110 115	
aag ccg ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag	483
Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln	
120 125 130 135	
cag tct ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc	531
Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser	
140 145 150	
tgc aag gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg	579
Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val	
155 160 165	
agg cag aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct	627
Arg Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro	
170 175 180	
gaa act ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata	675
Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile	
185 190 195	
gtg act gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc	723
Val Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser	
200 205 210 215	

ctg aca tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag 771
 Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu
 220 225 230

gac tgg ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct 819
 Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser
 235 240 245

cat cat cat cat cat cat tagggcctct ctggccgatt ccccgattt 867
 His His His His His His
 250

ccccgatcgt tcaaa 882

<210> 25
 <211> 339
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (1)..(339)

<400> 25
 cag gtt gtg atg acc cca aac cca ctc tcc ctg cct gtc agt ctt gga 48
 Gln Val Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val Ser Leu Gly
 1 5 10 15

gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt 96
 Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
 20 25 30

aat gga atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct 144
 Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca 192
 Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60

gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc 240
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt 288
 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
 85 90 95

aca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa 336
 Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

ggc 339
 Gly

<210> 26
 <211> 64
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 26

cccggggttg gattcggagc cagatcctga ggatttaccc tctgcagaga cagtgaccag 60
agtc 64

<210> 27

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 27

gagggtaaat cctcaggatc tggctccgaa tccaaaccg gggatgttgt gatgacccca 60
aac 63

<210> 28

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 28

gcactaggtc aagcggccgc ttactaatc agatcctctt ctgagatgag tttttcttct 60
tttattttcca gcttggtc 78

<210> 29

<211> 459

<212> DNA

<213> mouse

<220>

<221> CDS

<222> (19)..(459)

<220>

<221> mat_peptide

<222> (79)..(459)

<400> 29

gcactaggtc aatctaga atg gta agc gct att gtt tta tat gtg ctt ttg 51
Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu
-20 -15 -10

gcg gcg gcg gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct 99
Ala Ala Ala Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser
-5 -1 1 5

ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag	147
Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys	
10 15 20	
gct tgc ggc tac aca ttt act gac tat gaa ata cac tgg gtg agg cag	195
Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln	
25 30 35	
aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct gaa act	243
Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr	
40 45 50 55	
ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata gtg act	291
Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr	
60 65 70	
gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca	339
Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr	
75 80 85	
tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg	387
Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp	
90 95 100	
ggc caa ggg act ctg gtc act gtc tct gca gag ggt aaa tcc tca gga	435
Gly Gln Gly Thr Leu Val Thr Val Ser Ala Glu Gly Lys Ser Ser Gly	
105 110 115	
tct ggc tcc gaa tcc aaa ccc ggg	459
Ser Gly Ser Glu Ser Lys Pro Gly	
120 125	
<210> 30	
<211> 438	
<212> DNA	
<213> mouse	
<220>	
<221> CDS	
<222> (1)..(408)	
<400> 30	
gag ggt aaa tcc tca gga tct ggc tcc gaa tcc aaa ccc ggg gat gtt	48
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Pro Gly Asp Val	
1 5 10 15	
gtg atg acc cca aac cca ctc tcc ctg cct gtc agt ctt gga gat caa	96
Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln	
20 25 30	
gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt aat gga	144
Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly	
35 40 45	
atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct cca aag	192
Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys	
50 55 60	
ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg	240
Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg	

65	70	75	80	
ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc agc aga				288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg	85	90	95	
gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat				336
Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His	100	105	110	
gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa gaa gaa				384
Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Glu Glu	115	120	125	
aaa ctc atc tca gaa gag gat ctg aattagtaag gggccgcctt gacctagtgc				438
Lys Leu Ile Ser Glu Glu Asp Leu	130	135		

<210> 31
 <211> 830
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (7)..(813)

<220>
 <221> mat_peptide
 <222> (67)..(813)

<400> 31	
tctaga atg gta agc gct att gtt tta tat gtg ctt ttg gcg gcg gcg	48
Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala	
-20 -15 -10	

gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct ggg gct gag	96
Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser Gly Ala Glu	
-5 -1 1 5 10	

ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag gct tcg ggc	144
Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly	
15 20 25	

tac aca ttt act gac tat gaa ata cac tgg gtg agg cag aca cct gtg	192
Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln Thr Pro Val	
30 35 40	

cat ggc ctg gaa tgg att gga gct att gat cct gaa act ggt ggt act	240
His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr	
45 50 55	

gcc tac aat cag aag ttc aag gac aag gcc ata gtg act gta gac aaa	288
Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys	
60 65 70	

tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca tct gaa gac	336
Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp	
75 80 85 90	

tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg ggc caa ggg	384
Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly	
95 100 105	
act ctg gtc act gtc tct gca gag ggt aaa tcc tca gga tct ggc tcc	432
Thr Leu Val Thr Val Ser Ala Glu Gly Lys Ser Ser Gly Ser Gly Ser	
110 115 120	
gaa tcc aaa ccc ggg gat gtt gtg atg acc cca aac cca ctc tcc ctg	480
Glu Ser Lys Pro Gly Asp Val Val Met Thr Pro Asn Pro Leu Ser Leu	
125 130 135	
cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag	528
Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln	
140 145 150	
agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac ctg cag	576
Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln	
155 160 165 170	
aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga	624
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg	
175 180 185	
ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat	672
Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	
190 195 200	
ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga gtt tat	720
Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr	
205 210 215	
ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc	768
Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr	
220 225 230	
aag ctg gaa ata aaa gaa gaa aaa ctc atc tca gaa gag gat ctg	813
Lys Leu Glu Ile Lys Glu Glu Lys Leu Ile Ser Glu Glu Asp Leu	
235 240 245	
aattagtaag cggccgc	830

<210> 32
 <211> 269
 <212> PRT
 <213> mouse

<400> 32
 Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala Ala His
 -20 -15 -10 -5
 Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val
 -1 1 5 10
 Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly Tyr Thr
 15 20 25
 Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln Thr Pro Val His Gly
 30 35 40

Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr Ala Tyr
 45 50 55 60
 Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys Ser Ser
 65 70 75
 Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala
 80 85 90
 Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly Thr Leu
 95 100 105
 Val Thr Val Ser Ala Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser
 110 115 120
 Lys Pro Gly Asp Val Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val
 125 130 135 140
 Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
 145 150 155
 Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
 160 165 170
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
 175 180 185
 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 190 195 200
 Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
 205 210 215 220
 Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
 225 230 235
 Glu Ile Lys Glu Glu Lys Leu Ile Ser Glu Glu Asp Leu
 240 245

<210> 33
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:c-myc tag

<400> 33
 gaagaaaaac tcattcaga agaggatctg

30

<210> 34
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:p67 leader

<400> 34

atggtaagcg ctattgtttt atatgtgott ttggcggcgg cggcgcattc tgcctttgcg 60

<210> 35

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 35

gcactaggtc aatctagaat gactatcctt tgctggctgg cccttctgtc aactctgact 60

gccgtcaacg ctgcggttgt gatg

84

<210> 36

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 36

gcccttggtg ccctcgccgc tgcccggctt gccgctgccg ctggtgctgc cttttatttc 60

cagcttggtc

70

<210> 37

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 37

ggcagcacca gcggcagcgg caagccgggc agcggcgagg gcagcaccaa gggccaggtt 60

caactgcagc agtc

74

<210> 38

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 38

gcactaggtc aagcggccgc atgatgatga tgatgatgag aaccccgcat tgcagagaca 60

gtgaccagag tc

72

<210> 39

<211> 41

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 39
aaaatttgcg gccgcctaata gatgatgatg atgatgagaa c 41

<210> 40
<211> 462
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (19)..(462)

<220>
<221> mat_peptide
<222> (73)..(462)

<400> 40
gcactagggtc aatctaga atg act atc ctt tgc tgg cta gcc ctt ctg tca 51
Met Thr Ile Leu Cys Trp Leu Ala Leu Leu Ser
-15 -10

act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca aac cca ctc 99
Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro Asn Pro Leu
-5 -1 1 5

tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct 147
Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser
10 15 20 25

agt cag agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac 195
Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr
30 35 40

ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc 243
Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser
45 50 55

aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg 291
Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
60 65 70

aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga 339
Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
75 80 85

gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg 387
Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly
90 95 100 105

ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc aag ccg 435
Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro
110 115 120

ggc agc ggc gag ggc agc acc aag ggc 462

Gly Ser Gly Glu Gly Ser Thr Lys Gly
 125 130

<210> 41
 <211> 443
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (1)..(423)

<400> 41

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ggc agc acc agc ggc agc ggc aag ccg ggc agc ggc gag ggc agc acc 48
Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
  1             5             10             15

aag ggc cat gtt caa ctg cag cag tct ggg gct gag ctg gtg agg cct 96
Lys Gly His Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro
             20             25             30

ggg gct tca gtg acg ctg tcc tgc aag gct tcg ggc tac aca ttt act 144
Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
             35             40             45

gac tat gaa ata cac tgg gtg aag cag aca cct gtg cat ggc ctg gaa 192
Asp Tyr Glu Ile His Trp Val Lys Gln Thr Pro Val His Gly Leu Glu
             50             55             60

tgg att gga gct att gat cct gaa act ggt ggt act gcc tac aat cag 240
Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr Ala Tyr Asn Gln
             65             70             75             80

aag ttc aag gac aag gcc ata gtg act gta gac aaa tcc tcc agc aca 288
Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys Ser Ser Ser Thr
             85             90             95

gcc tac atg gag ctc cgc agc ctg aca tct gaa gac tct gcc gtc tat 336
Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
             100             105             110

tac tat aca aga tgg ttt gag gac tgg ggc caa ggg act ctg gtc act... 384
Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly Thr Leu Val Thr
             115             120             125

gtc tct gca atg cgg ggt tct cat cat cat cat cat cat gcggccgctt 433
Val Ser Ala Met Arg Gly Ser His His His His His His
             130             135             140

gacctagtgcc 443

```

<210> 42
 <211> 851
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (19)..(831)

<220>

<221> mat_peptide

<222> (73)..(831)

<400> 42

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gcactagggtc aatctaga atg act atc ctt tgc tgg cta gcc ctt ctg tca 51
               Met Thr Ile Leu Cys Trp Leu Ala Leu Leu Ser
                               -15                               -10

act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca aac cca ctc 99
Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro Asn Pro Leu
          -5                -1  1                5

tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct 147
Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser
  10                15                20                25

agt cag agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac 195
Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr
          30                35                40

ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc 243
Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser
          45                50                55

aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg 291
Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
          60                65                70

aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga 339
Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
          75                80                85

gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg 387
Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly
  90                95                100                105

ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc aag ccg 435
Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro
          110                115                120

ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag cag tct... 483
Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln Gln Ser
          125                130                135

ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag 531
Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys
          140                145                150

gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg aag cag 579
Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Lys Gln
          155                160                165

aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct gaa act 627
Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr
          170                175                180                185

ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata gtg act 675
Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr
          190                195                200
```

gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca 723
Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr
205 210 215

tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg 771
Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp
220 225 230

ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct cat cat 819
Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser His His
235 240 245

cat cat cat cat gcggccgctt gacctagtgc 851
His His His His
250

<210> 43
<211> 867
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (31)..(843)

<220>
<221> mat_peptide
<222> (85)..(843)

<400> 43
aatttaaacg gatcccggtt accttctaga atg act atc ctt tgc tgg cta gcc 54
Met Thr Ile Leu Cys Trp Leu Ala
-15

ctt ctg tca act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca 102
Leu Leu Ser Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro
-10 -5 -1 1 5

aac cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct 150
Asn Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
10 15 20

tgc aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta 198
Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu
25 30 35

cat tgg tac ctg cag aag cca gcc cag tct cca aag ctc ctg atc tac 246
His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
40 45 50

aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt 294
Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
55 60 65 70

gga tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag 342
Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu
75 80 85

gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg 390

Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Tyr	Thr		
			90					95					100				
ttc	gga	ggg	ggg	acc	aag	ctg	gaa	ata	aaa	ggc	agc	acc	agc	ggc	agc	438	
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser		
		105					110					115					
ggc	aag	ccg	ggc	agc	ggc	gag	ggc	agc	acc	aag	ggc	cat	gtt	caa	ctg	486	
Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	Thr	Lys	Gly	His	Val	Gln	Leu		
	120					125					130						
cag	cag	tct	ggg	gct	gag	ctg	gtg	agg	cct	ggg	gct	tca	gtg	acg	ctg	534	
Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala	Ser	Val	Thr	Leu		
135					140					145					150		
tcc	tgc	aag	gct	tcg	ggc	tac	aca	ttt	act	gac	tat	gaa	ata	cac	tgg	582	
Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Glu	Ile	His	Trp		
				155					160					165			
gtg	aag	cag	aca	cct	gtg	cat	ggc	ctg	gaa	tgg	att	gga	gct	att	gat	630	
Val	Lys	Gln	Thr	Pro	Val	His	Gly	Leu	Glu	Trp	Ile	Gly	Ala	Ile	Asp		
			170					175					180				
cct	gaa	act	ggg	ggg	act	gcc	tac	aat	cag	aag	ttc	aag	gac	aag	gcc	678	
Pro	Glu	Thr	Gly	Gly	Thr	Ala	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala		
		185					190					195					
ata	gtg	act	gta	gac	aaa	tcc	tcc	agc	aca	gcc	tac	atg	gag	ctc	cgc	726	
Ile	Val	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Arg		
	200					205					210						
agc	ctg	aca	tct	gaa	gac	tct	gcc	gtc	tat	tac	tat	aca	aga	tgg	ttt	774	
Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Tyr	Thr	Arg	Trp	Phe		
215				220					225					230			
gag	gac	tgg	ggc	caa	ggg	act	ctg	gtc	act	gtc	tct	gca	atg	cgg	ggg	822	
Glu	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Met	Arg	Gly		
			235					240					245				
tct	cat	cat	cat	cat	cat	cat	taggcggccg`ctgcagatct	gac								867	
Ser	His	His	His	His	His	His											
			250														

<210> 44

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 44

tttaaaggcc atattggcca tgactatcct ttgctggct

39

<210> 45

<211> 43

<212> DNA

<213> Artificial Sequence

ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc	387
Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe	
90 95 100	
gga ggg ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc	435
Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly	
105 110 115	
aag ccg ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag	483
Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln	
120 125 130 135	
cag tct ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc	531
Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser	
140 145 150	
tgc aag gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg	579
Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val	
155 160 165	
agg cag aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct	627
Arg Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro	
170 175 180	
gaa act ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata	675
Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile	
185 190 195	
gtg act gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc	723
Val Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser	
200 205 210 215	
ctg aca tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag	771
Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu	
220 225 230	
gac tgg ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct	819
Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser	
235 240 245	
cat cat cat cat cat cat tagggcctct ctggccgac ccccgaaattt	867
His His His His His His	
250	
ccccgatcgt tcaaa	882

<210> 48
 <211> 846
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (25)..(786)

<400> 48	
ctgcagggta cggccatatt ggcc atg gat gtt gtg atg acc cca aac cca	51
Met Asp Val Val Met Thr Pro Asn Pro	
1 5	

ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga	99
Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg	
10 15 20 25	
tct agt cag agc ctt tta cac agt aat gga atc acc tat tta cat tgg	147
Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp	
30 35 40	
tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt	195
Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val	
45 50 55	
tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca	243
Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser	
60 65 70	
ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg	291
Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu	
75 80 85	
gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga	339
Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly	
90 95 100 105	
ggg ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc aag	387
Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys	
110 115 120	
ccg ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag cag	435
Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln Gln	
125 130 135	
tct ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc	483
Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys	
140 145 150	
aag gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg agg	531
Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg	
155 160 165	
cag aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct gaa	579
Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu	
170 175 180 185	
act ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata gtg	627
Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val	
190 195 200	
act gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg	675
Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu	
205 210 215	
aca tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag gac	723
Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp	
220 225 230	
tgg ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct cat	771
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser His	
235 240 245	
cat cat cat cat cat tagggcctct ctggccgata ccccgaaattt ccccgatcgt	826

His His His His His
250

tcaaacattt ggcaataaag

846

<210> 49
<211> 738
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (19)..(687)
<223> mature peptide is coded by nucleotides 49 to 687

<400> 49
cccgggtacc cttctaga ctc gtg aca gtt gtt gat ggt gcc caa tcc cag 51
Leu Val Thr Val Val Asp Gly Ala Gln Ser Gln
1 5 10

gtt caa ctg cag cag tct ggg gct gag ctg gtg agg cct ggg gct tca 99
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser
15 20 25

gtg acg ctg tcc tgc aag gct tcg ggc tac aca ttt act gac tat gaa 147
Val Thr Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu
30 35 40

ata cac tgg gtg agg cag aca cct gtg cat ggc ctg gaa tgg att gga 195
Ile His Trp Val Arg Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly
45 50 55

gct att gat cct gaa act ggt ggt act gcc tac aat cag aag ttc aag 243
Ala Ile Asp Pro Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys
60 65 70 75

gac aag gcc ata gtg act gta gac aaa tcc tcc agc aca gcc tac atg 291
Asp Lys Ala Ile Val Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
80 85 90

gag ctc cgc agc ctg aca tct gaa gac tct gcc gtc tat tac tat aca 339
Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr
95 100 105

aga tgg ttt gag gac tgg ggc caa ggg act ctg gtc act gtc tct gca 387
Arg Trp Phe Glu Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
110 115 120

gcc aaa aca aca ccc cca tca gtc tat cca ctg gcc cct ggg tgt gga 435
Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Cys Gly
125 130 135

gat aca act ggt tcc tct gtg act ctg gga tgc ctg gtc aag ggc tac 483
Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
140 145 150 155

ttc cct gag tca gtg act gtg act tgg aac tct gga tcc ctg tcc agc 531
Phe Pro Glu Ser Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
160 165 170

agt gtg cac acc ttc cca gct ctc ctg cag tct gga ctc tac act atg 579
 Ser Val His Thr Phe Pro Ala Leu Leu Gln Ser Gly Leu Tyr Thr Met
 175 180 185

agc agc tca gtg act gtc ccc tcc agc acc tgg cca agt cag acc gtc 627
 Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Gln Thr Val
 190 195 200

acc tgc agc gtt gct cac cca gcc agc agc acc acg gtg gac aaa aaa 675
 Thr Cys Ser Val Ala His Pro Ala Ser Ser Thr Thr Val Asp Lys Lys
 205 210 215

ctt gag ccc agc gcggccgctg caggtcttga tcctttcctg ggacccggca 727
 Leu Glu Pro Ser
 220

agaaccacaaa a 738

<210> 50
 <211> 42
 <212> DNA
 <213> mouse

<400> 50
 gcactagggtc aagcggccgc ttactaacac tcattcctgt tg 42

<210> 51
 <211> 753
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (7)..(705)

<220>
 <221> mat_peptide
 <222> (67)..(705)

<400> 51
 tctaga atg gta agc gct att gtt tta tat gtg ctt ttg gcg gcg gcg... 48
 Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala
 -20 -15 -10

gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct ggg gct gag 96
 Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser Gly Ala Glu
 -5 -1 1 5 10

ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag gct tgc ggc 144
 Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly
 15 20 25

tac aca ttt act gac tat gaa ata cac tgg gtg agg cag aca cct gtg 192
 Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln Thr Pro Val
 30 35 40

cat ggc ctg gaa tgg att gga gct att gat cct gaa act ggt ggt act 240
 His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr
 45 50 55

gcc tac aat cag aag ttc aag gac aag gcc ata gtg act gta gac aaa	288
Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys	
60 65 70	
tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca tct gaa gac	336
Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp	
75 80 85 90	
tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg ggc caa ggg	384
Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly	
95 100 105	
act ctg gtc act gtc tct gca gcc aaa aca aca ccc cca tca gtc tat	432
Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val Tyr	
110 115 120	
cca ctg gcc cct ggg tgt gga gat aca act ggt tcc tct gtg act ctg	480
Pro Leu Ala Pro Gly Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu	
125 130 135	
gga tgc ctg gtc aag ggc tac ttc cct gag tca gtg act gtg act tgg	528
Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Ser Val Thr Val Thr Trp	
140 145 150	
aac tct gga tcc ctg tcc agc agt gtg cac acc ttc cca gct ctc ctg	576
Asn Ser Gly Ser Leu Ser Ser Ser Val His Thr Phe Pro Ala Leu Leu	
155 160 165 170	
cag tct gga ctc tac act atg agc agc tca gtg act gtc ccc tcc agc	624
Gln Ser Gly Leu Tyr Thr Met Ser Ser Ser Val Thr Val Pro Ser Ser	
175 180 185	
acc tgg acc tgc agc gtt gct cac cca gcc agc agc cca agt cag acc	672
Thr Trp Thr Cys Ser Val Ala His Pro Ala Ser Ser Pro Ser Gln Thr	
190 195 200	
gtc acc acg gtg gac aaa aaa ctt gag ccc agc tagtaatgag cggccgctgc	725
Val Thr Thr Val Asp Lys Lys Leu Glu Pro Ser	
205 210	

agatctgatac ctttcctggg acccgga 753

<210> 52

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:nt 2253 to 2271
of pDAB439

<400> 52

tgcatgtgtt ctccttttt

19

<210> 53

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:nt 4256 to 4308
of pDAB439

<400> 53

ggtacggcca tattggccga gctcggcctc tctggccgat cccc

44

<210> 54

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:nt 4744 to 4807
of pDAB439

<400> 54

gcggccgctt taacgcccg gcattttaa ggcgcgccgc gatcgcttgc agatctgcat 60

ggg

63

<210> 55

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:nt 5417 to 5436
of pDAB439

<400> 55

ggggactcta gaggatccag

20

<210> 56

<211> 24

<212> PRT

<213> Zea mays

<400> 56

Pro Gly Ser Pro Ala Pro Ala Ala Pro Lys Asn Gly Leu Gly Glu Arg...
1 5 10 15

Pro Glu Ser Leu Asp Val Arg Gly
20